Freeform Search

Database: US Pre-Grant Publication Full-Text Database; US Patents Full-Text Database; US OCR Full-Text Database; EPO Abstracts Database; JPO Abstracts Database; Derwent World Patents Index; IBM Technical Disclosure Bulletins

Term: identif$7 same probabilit$3 same allele same control same (contaminat$3 or sutter or allele dropout)

Display: 10 **Documents in Display Format:** - **Starting with Number** 11

Generate: ○ **Hit List** ◉ **Hit Count** ○ **Side by Side** ○ **Image**

Search Clear Interrupt

Search History

DATE: Thursday, April 22, 2004 Printable Copy Create Case

Set Name side by side	Query	Hit Count	Set Name result set
DB=USPT,EPAB,JPAB,DWPI; PLUR=YES; OP=ADJ			
L12	identif$7 same probabilit$3 same allele same control same (contaminat$3 or sutter or allele dropout)	0	L12
L11	l7 and (populat$3 or loc$2 or allele$1 or DNA)	19	L11
L10	anL9	0	L10
L9	L8	0	L9
L8	l1 and (identif$7 near5 populat$3)	0	L8
L7	l1 and identif$7	45	L7
L6	l1 and identif$7 DNA	0	L6
L5	L4 and identif$7 loc$2	0	L5
L4	l1 and (identif$7 near5 (allele or loc$2))	0	L4
L3	L2	0	L3
L2	L1 and (identif$7 (allele or loc$2))	0	L2
L1	probabilit$3 same (contaminat$3 or stutter or allele dropout) same control	92	L1

END OF SEARCH HISTORY

09/834822

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* * * * * * * * * * * * * * STN  Columbus  * * * * * * * * * * * * * * *

FILE 'HOME' ENTERED AT 16:33:45 ON 22 APR 2004

=> file medline caplus embase biosis
COST IN U.S. DOLLARS                                  SINCE FILE      TOTAL
                                                         ENTRY    SESSION
FULL ESTIMATED COST                                       0.21       0.21

FILE 'MEDLINE' ENTERED AT 16:34:03 ON 22 APR 2004

FILE 'CAPLUS' ENTERED AT 16:34:03 ON 22 APR 2004
USE IS SUBJECT TO THE TERMS OF YOUR STN CUSTOMER AGREEMENT.
PLEASE SEE "HELP USAGETERMS" FOR DETAILS.
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FILE 'BIOSIS' ENTERED AT 16:34:03 ON 22 APR 2004
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=> s probabilit###(P)identif#####(p)(allele or loc## or DNA or population)
L1        5409 PROBABILIT###(P) IDENTIF#####(P)(ALLELE OR LOC## OR DNA OR POPUL
               ATION)

=> s l1 and control
L2         822 L1 AND CONTROL

=> s l2 and likelihood ratio
L3           5 L2 AND LIKELIHOOD RATIO

=> dup rem l3
PROCESSING COMPLETED FOR L3
L4             3 DUP REM L3 (2 DUPLICATES REMOVED)

=> d l4 1-3 bib ab kwic\
'KWIC\' IS NOT A VALID FORMAT FOR FILE 'MEDLINE'

The following are valid formats:

The default display format is BIB.

ABS ---- AB
ALL ---- AN, DN, TI, CM, AU, CS, NC, SO, CY, DT, LA, FS, OS, EM,
         ED, AB, ST, CT, NA, RN, CN, GEN
BIB ---- AN, DN, TI, CM, AU, CS, NC, SO, CY, DT, LA, FS, OS, EM, ED
CBIB --- AN, DN, TI, CM, AU, CS, NC, SO, CY, DT, LA, FS, OS, EM, ED
DALL --- ALL, delimited for post processing
IABS --- ABS, with a text label
IALL --- ALL, indented with text labels
IBIB --- BIB, indented with text labels
IND ---- ST, CT, NA, RN, CN, GEN
SAM ---- TI, CM, ST, CT, NA, RN, CN, GEN
TRI ---- TI, CM, ST, CT, NA, RN, CN, GEN
TRIAL -- TI, CM, ST, CT, NA, RN, CN, GEN
HIT ---- All fields containing hit terms
HITIND - IND
KWIC --- All hit terms plus 20 words on either side
OCC ---- List of display fields containing hit terms

Hit terms will be highlighted in all available fields except CM and
PY.
```

To display a particular field or fields, enter the display field codes. For a list of display field codes, enter 'HELP DFIELDS' at an arrow prompt (=>). Examples of formats include: 'BIB'; 'AB'; 'SO,ST'. You may specify the format fields in any order, and the information will be displayed in the same order as the format specification.

The same formats (except for HIT, HITIND, KWIC, and OCC) may be used with the DISPLAY ACC command to display the record for a specified Accession Number.
ENTER DISPLAY FORMAT (BIB):end

=> d l4 1-3 bib ab kwic

L4 ANSWER 1 OF 3 MEDLINE on STN
AN 2001102294 MEDLINE
DN PubMed ID: 10977068
TI Analysis of gene expression microarrays for phenotype classification.
AU Califano A; Stolovitzky G; Tu Y
CS IBM Computational Biology Center, T.J. Watson Research Center, Yorktown Heights, NY 10598, USA.. acal@us.ibm.com
SO Proceedings / ... International Conference on Intelligent Systems for Molecular Biology ; ISMB. International Conference on Intelligent Systems for Molecular Biology, (2000) 8 75-85.
Journal code: 9509125.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 200101
ED Entered STN: 20010322
Last Updated on STN: 20010322
Entered Medline: 20010126
AB Several microarray technologies that monitor the level of expression of a large number of genes have recently emerged. Given **DNA** -microarray data for a set of cells characterized by a given phenotype and for a set of **control** cells, an important problem is to **identify** "patterns" of gene expression that can be used to predict cell phenotype. The potential number of such patterns is exponential in the number of genes. In this paper, we propose a solution to this problem based on a supervised learning algorithm, which differs substantially from previous schemes. It couples a complex, non-linear similarity metric, which maximizes the **probability** of discovering discriminative gene expression patterns, and a pattern discovery algorithm called SPLASH. The latter discovers efficiently and deterministically all statistically significant gene expression patterns in the phenotype set. Statistical significance is evaluated based on the **probability** of a pattern to occur by chance in the **control** set. Finally, a greedy set covering algorithm is used to select an optimal subset of statistically significant patterns, which form the basis for a standard **likelihood ratio** classification scheme. We analyze data from 60 human cancer cell lines using this method, and compare our results with those of other supervised learning schemes. Different phenotypes are studied. These include cancer morphologies (such as melanoma), molecular targets (such as mutations in the p53 gene), and therapeutic targets related to the sensitivity to an anticancer compounds. We also analyze a synthetic data set that shows that this technique is especially well suited for the analysis of sub-phenotype mixtures. For complex phenotypes, such as p53, our method produces an encouragingly low rate of false positives and false negatives and seems to outperform the others. Similar low rates are reported when predicting the efficacy of experimental anticancer compounds. This counts among the first reported studies where drug efficacy has been successfully predicted from large-scale expression data analysis.

AB Several microarray technologies that monitor the level of expression of a large number of genes have recently emerged. Given **DNA** -microarray data for a set of cells characterized by a given phenotype and for a set of **control** cells, an important problem is to **identify** "patterns" of gene expression that can be used to predict cell phenotype. The potential number of such patterns is exponential. . . a supervised learning algorithm, which differs substantially from previous schemes. It couples a complex, non-linear similarity metric, which maximizes the **probability** of discovering discriminative gene expression patterns, and a pattern discovery algorithm called SPLASH. The latter discovers efficiently and deterministically all statistically significant gene expression patterns in the phenotype set. Statistical significance is evaluated based on the **probability** of a pattern to occur by chance in the **control** set. Finally, a greedy set covering algorithm is used to select an optimal subset of statistically significant patterns, which form the basis for a standard **likelihood ratio** classification scheme. We analyze data from 60 human cancer cell lines using this method, and compare our results with those. . .

L4 ANSWER 2 OF 3 MEDLINE on STN
AN 1999289975 MEDLINE
DN PubMed ID: 10361624
TI Use of sexually transmitted disease risk assessment algorithms for selection of intrauterine device candidates.
AU Morrison C S; Sekadde-Kigondu C; Miller W C; Weiner D H; Sinei S K
CS Family Health International, Research Triangle Park, North Carolina 27709, USA.. emorrison@fhi.org
SO Contraception, (1999 Feb) 59 (2) 97-106.
Journal code: 0234361. ISSN: 0010-7824.
Report No.: PIP-142740; POP-00288104.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals; Population; AIDS
EM 199907
ED Entered STN: 19990806
Last Updated on STN: 20021101
Entered Medline: 19990723
AB Sexually transmitted diseases (STD) are an important contraindication for intrauterine device (IUD) insertion. Nevertheless, laboratory testing for STD is not possible in many settings. The objective of this study is to evaluate the use of risk assessment algorithms to predict STD and subsequent IUD-related complications among IUD candidates. Among 615 IUD users in Kenya, the following algorithms were evaluated: 1) an STD algorithm based on US Agency for International Development (USAID) Technical Working Group guidelines: 2) a Centers for Disease **Control** and Prevention (CDC) algorithm for management of chlamydia; and 3) a data-derived algorithm modeled from study data. Algorithms were evaluated for prediction of chlamydial and gonococcal infection at 1 month and complications (pelvic inflammatory disease [PID], IUD removals, and IUD expulsions) over 4 months. Women with STD were more likely to develop complications than women without STD (19% vs 6%; risk ratio = 2.9; 95% CI 1.3-6.5). For STD prediction, the USAID algorithm was 75% sensitive and 48% specific, with a positive **likelihood ratio** (LR+) of 1.4. The CDC algorithm was 44% sensitive and 72% specific, LR+ = 1.6. The data-derived algorithm was 91% sensitive and 56% specific, with LR+ = 2.0 and LR- = 0.2. Category-specific LR for this algorithm **identified** women with very low (< 1%) and very high (29%) infection **probabilities**. The data-derived algorithm was also the best predictor of IUD-related complications. These results suggest that use of STD algorithms may improve selection of IUD users. Women at high risk for STD could be counseled to avoid IUD, whereas women at moderate risk should be monitored closely and counseled to use condoms.

This study aimed to evaluate the effectiveness of using risk assessment algorithms in predicting sexually transmitted disease (STD) and subsequent IUD-related complications among IUD candidates. The study **population** was selected among women who desired an IUD insertion in Nairobi, Kenya. The following algorithms drawn from the study of IUD use and HIV infection among these 615 IUD users were evaluated: 1) an STD algorithm based on US Agency for International Development (USAID) Technical Working Group guidelines; 2) a Centers for Disease **Control** and Prevention (CDC) algorithm for management of chlamydia; 3) a data-derived algorithm modeled from data. Algorithms were also evaluated for prediction of chlamydial and gonococcal infection at 1 month and complications (pelvic inflammatory disease, IUD removals, and IUD expulsions) at 4 months. Results showed that women with STDs were more likely to develop complications than women without STDs (19% vs. 6% risk ratio = 2.9; 95% CI, 1.3-6.5). In STD prediction, the USAID algorithm was 91% sensitive and 56% specific, with LR+ = 2.0 and LR- = 0.2. Category-specific LR for this algorithm **identified** women with very low (1%) and very high (29%) infection **probabilities**. Thus, sexually transmitted disease was associated with increased risk for complications after IUD insertion. Moreover, it may be concluded that simple risk assessment criteria can assist in the identification of women at high and low risk for STD among women presenting for IUD insertion; it may also be concluded that the use of simple risk assessment tools may facilitate the identification of women who require close observation, thus reducing the incidence of IUD-related complications.

AB . . . an STD algorithm based on US Agency for International Development (USAID) Technical Working Group guidelines: 2) a Centers for Disease **Control** and Prevention (CDC) algorithm for management of chlamydia; and 3) a data-derived algorithm modeled from study data. Algorithms were evaluated. . . = 2.9; 95% CI 1.3-6.5). For STD prediction, the USAID algorithm was 75% sensitive and 48% specific, with a positive **likelihood ratio** (LR+) of 1.4. The CDC algorithm was 44% sensitive and 72% specific, LR+ = 1.6. The data-derived algorithm was 91% sensitive and 56% specific, with LR+ = 2.0 and LR- = 0.2. Category-specific LR for this algorithm **identified** women with very low (< 1%) and very high (29%) infection **probabilities** . The data-derived algorithm was also the best predictor of IUD-related complications. These results suggest that use of STD algorithms may. . . of using risk assessment algorithms in predicting sexually transmitted disease (STD) and subsequent IUD-related complications among IUD candidates. The study **population** was selected among women who desired an IUD insertion in Nairobi, Kenya. The following algorithms drawn from the study of. . . an STD algorithm based on US Agency for International Development (USAID) Technical Working Group guidelines; 2) a Centers for Disease **Control** and Prevention (CDC) algorithm for management of chlamydia; 3) a data-derived algorithm modeled from data. Algorithms were also evaluated for. . . algorithm was 91% sensitive and 56% specific, with LR+ = 2.0 and LR- = 0.2. Category-specific LR for this algorithm **identified** women with very low (1%) and very high (29%) infection **probabilities**. Thus, sexually transmitted disease was associated with increased risk for complications after IUD insertion. Moreover, it may be concluded that. . .

CT Check Tags: Female; Human; Support, Non-U.S. Gov't
Adult
Algorithms
Centers for Disease Control and Prevention (U.S.)
HIV Infections: EP, epidemiology
HIV Infections: PC, prevention & control
HIV Infections: TM, transmission
*Intrauterine Devices
Kenya
*Patient Selection
Risk Assessment
Risk Factors

*Sexually Transmitted Diseases: EP, epidemiology
Sexually Transmitted Diseases: PC, prevention & control
*Sexually Transmitted Diseases: TM, transmission
United States

L4 ANSWER 3 OF 3 MEDLINE on STN DUPLICATE 1
AN 89235521 MEDLINE
DN PubMed ID: 2523948
TI Sensitivity study of H-reflex alterations in idiopathic low back pain patients vs. a healthy population.
CM Comment in: J Manipulative Physiol Ther. 1989 Dec;12(6):497-8. PubMed ID: 2534130
Comment in: J Manipulative Physiol Ther. 1991 Feb;14(2):154-8. PubMed ID: 1826923
Erratum in: J Manipulative Physiol Ther 1989 Oct;12(5):followi
AU Humphreys C R; Triano J J; Brandl M J
CS Spinal Ergonomics and Joint Laboratory, National College Chiropractic, Lombard, IL 60148.
SO Journal of manipulative and physiological therapeutics, (1989 Apr) 12 (2) 71-8.
Journal code: 7807107. ISSN: 0161-4754.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 198906
ED Entered STN: 19900306
Last Updated on STN: 19900306
Entered Medline: 19890612
AB Twenty-seven male and 12 female healthy volunteers were tested twice with 2-7 days separation. Hoffman (H) reflexes and muscle (M) activation waves were obtained from the posterior tibial nerves bilaterally. Results were compared to those obtained from patients presenting with a complaint of low back and/or leg pain, without compressive neuropathy. M, F, H latencies and H/Mmax ratio were recorded. H/M ratio and latency comparisons were not significantly different in the **control** group left to right or test to test. For the low back pain group, 10-14 days following the initial evaluation, each subject returned for a follow-up test. During the interim, the patient was followed conservatively using manipulation and home care. Analysis of variance (ANOVA) testing of ratio values demonstrated a difference in overall mean values (p greater than 0.001) for comparisons between the **control** (mean = 0.367), pretest (mean = 0.695), and posttest (mean = 0.558) values. Sensitivity in discriminating acute low back pain subjects from healthy controls was tested by determining the distance between mean H/M values for the **probability** curves of each **population**, with an arbitrary cutoff value of 0.6 as the upper limit normal. Sensitivity distance was 2.29 with a **likelihood ratio** of 3.04. This suggests that an H/Mmax ratio greater than or equal to 0.6 will correctly **identify** two of three patients with idiopathic low back pain.
AB . . . M, F, H latencies and H/Mmax ratio were recorded. H/M ratio and latency comparisons were not significantly different in the **control** group left to right or test to test. For the low back pain group, 10-14 days following the initial evaluation,. . . (ANOVA) testing of ratio values demonstrated a difference in overall mean values (p greater than 0.001) for comparisons between the **control** (mean = 0.367), pretest (mean = 0.695), and posttest (mean = 0.558) values. Sensitivity in discriminating acute low back pain subjects from healthy controls was tested by determining the distance between mean H/M values for the **probability** curves of each **population**, with an arbitrary cutoff value of 0.6 as the upper limit normal. Sensitivity distance was 2.29 with a **likelihood ratio** of 3.04.
This suggests that an H/Mmax ratio greater than or equal to 0.6 will

correctly **identify** two of three patients with idiopathic low back pain.

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